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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2009; month=3; day=24; hr=15; min=1; sec=14; ms=491;]

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Reviewer Comments:

<210> 8

<211> 139

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: partial
sequence of pGEX2ThCD83ext

<400> 8

Per the above sequence id# 8, please insert <220>, whenever numeric identifiers <221>, <222> or <223> is present. Please correct the remaining sequences showing similar errors. Please also correct <160> response, there were a total of 13 sequences found not 12.

Ser Pro Asn Lys His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu

195

200

205

Val

209

The above is a sample of invalid amino acid numbering also appearing in sequence id# 13. Please number amino acids every 5th base.

Application No: 10535522 Version No: 2.0

Input Set:

Output Set:

Started: 2009-03-02 13:23:43.501
Finished: 2009-03-02 13:23:44.828
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 327 ms
Total Warnings: 8
Total Errors: 6
No. of SeqIDs Defined: 12
Actual SeqID Count: 13

Error code	Error Description
E 201	Mandatory field data missing in <140>
E 201	Mandatory field data missing in <141>
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
E 323	Invalid/missing amino acid numbering SEQID (13)at Protein (209)
E 252	Calc# of Seq. differs from actual; 12 seqIds defined; count=13

SEQUENCE LISTING

<110> Steinkasserer, Alexander

<120> Use of Soluble Forms of CD83 and Nucleic Acids Encoding
them for the Treatment or Prevention of Diseases

<130> 032723woJH

<140> 10535522

<141> 2006-04-13

<160> 12

<170> PatentIn Ver. 2.1

<210> 1

<211> 618

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(615)

<400> 1

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Met	Ser	Arg	Gly	Leu	Gln	Leu	Leu	Leu	Leu	Ser	Cys	Ala	Tyr	Ser	Leu	
1				5					10					15		

gct	ccc	gcg	acg	ccg	gag	gtg	aag	gtg	gct	tgc	tcc	gaa	gat	gtg	gac	96
Ala	Pro	Ala	Thr	Pro	Glu	Val	Lys	Val	Ala	Cys	Ser	Glu	Asp	Val	Asp	
			20					25					30			

ttg	ccc	tgc	acc	gcc	ccc	tgg	gat	ccg	cag	gtt	ccc	tac	acg	gtc	tcc	144
Leu	Pro	Cys	Thr	Ala	Pro	Trp	Asp	Pro	Gln	Val	Pro	Tyr	Thr	Val	Ser	
		35					40					45				

tgg	gtc	aag	tta	ttg	gag	ggt	ggt	gaa	gag	agg	atg	gag	aca	ccc	cag	192
Trp	Val	Lys	Leu	Leu	Glu	Gly	Gly	Glu	Glu	Arg	Met	Glu	Thr	Pro	Gln	
	50					55				60						

gaa	gac	cac	ctc	agg	gga	cag	cac	tat	cat	cag	aag	ggg	caa	aat	ggt	240
Glu	Asp	His	Leu	Arg	Gly	Gln	His	Tyr	His	Gln	Lys	Gly	Gln	Asn	Gly	
65					70					75				80		

tct	ttc	gac	gcc	ccc	aat	gaa	agg	ccc	tat	tcc	ctg	aag	atc	cga	aac	288
Ser	Phe	Asp	Ala	Pro	Asn	Glu	Arg	Pro	Tyr	Ser	Leu	Lys	Ile	Arg	Asn	
			85					90						95		

act	acc	agc	tgc	aac	tcg	ggg	aca	tac	agg	tgc	act	ctg	cag	gac	ccg	336
Thr	Thr	Ser	Cys	Asn	Ser	Gly	Thr	Tyr	Arg	Cys	Thr	Leu	Gln	Asp	Pro	
			100					105					110			

gat	ggg	cag	aga	aac	cta	agt	ggc	aag	gtg	atc	ttg	aga	gtg	aca	gga	384
Asp	Gly	Gln	Arg	Asn	Leu	Ser	Gly	Lys	Val	Ile	Leu	Arg	Val	Thr	Gly	
		115					120					125				

tgc	cct	gca	cag	cgt	aaa	gaa	gag	act	ttt	aag	aaa	tac	aga	gcg	gag	432
Cys	Pro	Ala	Gln	Arg	Lys	Glu	Glu	Thr	Phe	Lys	Lys	Tyr	Arg	Ala	Glu	

130	135	140	
att gtc ctg ctg ctg gct ctg gtt att ttc tac tta aca ctc atc att	480		
Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile			
145	150	155	160
ttc act tgt aag ttt gca cgg cta cag agt atc ttc cca gat ttt tct	528		
Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser			
165	170	175	
aaa gct ggc atg gaa cga gct ttt ctc cca gtt acc tcc cca aat aag	576		
Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys			
180	185	190	
cat tta ggg cta gtg act cct cac aag aca gaa ctg gta tga	618		
His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu Val			
195	200	205	
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<211> 205			
<212> PRT			
<213> Homo sapiens			
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Ala Pro Ala Thr Pro Glu Val Lys Val Ala Cys Ser Glu Asp Val Asp			
20	25	30	
Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser			
35	40	45	
Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln			
50	55	60	
Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly			
65	70	75	80
Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn			
85	90	95	
Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro			
100	105	110	
Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly			
115	120	125	
Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu			
130	135	140	
Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile			
145	150	155	160
Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser			
165	170	175	

Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys
180 185 190

His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu Val
195 200 205

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<211> 2051
<212> DNA
<213> Mus musculus
<220>
<221> CDS
<222> (14)..(601)

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Met Ser Gln Gly Leu Gln Leu Leu Phe Leu Gly Cys
1 5 10
gcc tgc agc ctg gca ccc gcg atg gcg atg cgg gag gtg acg gtg gct 97
Ala Cys Ser Leu Ala Pro Ala Met Ala Met Arg Glu Val Thr Val Ala
15 20 25
tgc tcc gag acc gcc gac ttg cct tgc aca gcg ccc tgg gac ccg cag 145
Cys Ser Glu Thr Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln
30 35 40
ctc tcc tat gca gtg tcc tgg gcc aag gtc tcc gag agt ggc act gag 193
Leu Ser Tyr Ala Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu
45 50 55 60
agt gtg gag ctc ccg gag agc aag caa aac agc tcc ttc gag gcc ccc 241
Ser Val Glu Leu Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro
65 70 75
agg aga agg gcc tat tcc ctg acg atc caa aac act acc atc tgc agc 289
Arg Arg Arg Ala Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser
80 85 90
tcg ggc acc tac agg tgt gcc ctg cag gag ctc gga ggg cag cgc aac 337
Ser Gly Thr Tyr Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn
95 100 105
ttg agc ggc acc gtg gtt ctg aag gtg aca gga tgc ccc aag gaa gct 385
Leu Ser Gly Thr Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala
110 115 120
aca gag tca act ttc agg aag tac agg gca gaa gct gtg ttg ctc ttc 433
Thr Glu Ser Thr Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe
125 130 135 140
tct ctg gtt gtt ttc tac ctg aca ctc atc att ttc acc tgc aaa ttt 481
Ser Leu Val Val Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe
145 150 155

gca cga cta caa agc att ttc cca gat att tct aaa cct ggt acg gaa 529
Ala Arg Leu Gln Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu
160 165 170

caa gct ttt ctt cca gtc acc tcc cca agc aaa cat ttg ggg cca gtg 577
Gln Ala Phe Leu Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val
175 180 185

acc ctt cct aag aca gaa acg gta tgagtaggat ctccactggt ttttaciaaag 631
Thr Leu Pro Lys Thr Glu Thr Val
190 195

ccaagggcac atcagatcag tgtgcttgaa tgccacccgg acaagagaag aatgagctcc 691

atcctcagat ggcaaccttt ctttgaagtc cttcacctga cagtgggctc cacactactc 751

cctgacacag ggtcttgagc accatcatat gatcacgaag catggagtat caccgcttct 811

ctgtggctgt cagcttaatg tttcatgtgg ctatctggtc aacctcgtga gtgcttttca 871

gtcatctaca agctatggtg agatgcaggt gaagcagggg catgggaaat ttgaacactc 931

tgagctggcc ctgtgacaga ctctgagga cagctgtcct ctctacatc tgggatacat 991

ctctttgaat ttgtcctgtt tcgttgcacc agcccagatg tctcacatct ggcggaatt 1051

gacaggccaa gctgtgagcc agtgggaaat atttagcaaa taatttccca gtgcgaaggt 1111

cctgctatta gtaaggagta ttatgtgtac atagaaatga gaggtcagtg aactattccc 1171

cagcagggcc ttttcatctg gaaaagacat ccacaaaagc agcaatacag agggatgcca 1231

catttatttt tttaatcttc atgtacttgt caaagaagaa ttttcatgt tttttcaaag 1291

aagtgtgttt ctttcctttt ttaaaatatg aaggctcagtg tacatagcat tgctagctga 1351

caagcagcct gagagaagat ggagaatgtt cctcaaaata gggacagcaa gctagaagca 1411

ctgtacagtg cctgctggg aagggcagac aatggactga gaaaccagaa gtctggccac 1471

aagattgtct gtatgattct ggacgagtca cttgtgggtt tcactctctg gttagtaaac 1531

cagatagttt agtctgggtt gaatacaatg gatgtgaagt tgcttgggga aagctgaatg 1591

tagtgaatac attggcaact ctactgggct gttaccttgt tgatatacta gagttctgga 1651

gctgagcgaa tgctgtcat atctcagctt gcccatcaat ccaaacacag gaggtacaa 1711

aaaggacatg agcatgggtc tctgtgtgaa ctctcctga gaaacgtgga gactggtca 1771

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tgcgccacga caggaggaag ttctcagatg ttgcattgat gtaacattgt tgcatttctt 1891

taatgagctg ggctccttcc tcatttgctt ccaaagaga ttttgtcca ctaatggtgt 1951

gcccatcacc cacactatga aagtaaaagg gatgctgagc agatacagcg tgcttacctc 2011

tcagccatga ctttcatgct attaaaagaa tgcatgtgaa 2051

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<211> 196

<212> PRT

<213> Mus musculus

<400> 4

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20 25 30

Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Leu Ser Tyr Ala
35 40 45

Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu Ser Val Glu Leu
50 55 60

Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro Arg Arg Arg Ala
65 70 75 80

Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser Ser Gly Thr Tyr
85 90 95

Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn Leu Ser Gly Thr
100 105 110

Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala Thr Glu Ser Thr
115 120 125

Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe Ser Leu Val Val
130 135 140

Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe Ala Arg Leu Gln
145 150 155 160

Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu Gln Ala Phe Leu
165 170 175

Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val Thr Leu Pro Lys
180 185 190

Thr Glu Thr Val
195

<210> 5

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for CD83ext

<400> 5

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<210> 6

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for CD83ext

<400> 6

aattagaatt ctcaaattctc cgctctgtat t 31

<210> 7

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: partial
sequence of pGEX2ThCD83ext

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<221> CDS

<222> (1)..(417)

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<222> (28)..(417)

<400> 7

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-5 -1 1 5

gtg aag gtg gct tgc tcc gaa gat gtg gac ttg ccc tgc acc gcc ccc 96
Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro
10 15 20

tgg gat ccg cag gtt ccc tac acg gtc tcc tgg gtc aag tta ttg gag 144
Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu
25 30 35

ggg ggt gaa gag agg atg gag aca ccc cag gaa gac cac ctc agg gga 192
Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
40 45 50 55

cag cac tat cat cag aag ggg caa aat ggt tct ttc gac gcc ccc aat 240
Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
60 65 70

gaa agg ccc tat tcc ctg aag atc cga aac act acc agc tgc aac tcg 288
Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
75 80 85

ggg aca tac agg tgc act ctg cag gac ccg gat ggg cag aga aac cta 336

Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
90 95 100

agt ggc aag gtg atc ttg aga gtg aca gga tgc cct gca cag cgt aaa 384
Ser Gly Lys Val Ile Leu Arg Val Thr Gly Cys Pro Ala Gln Arg Lys
105 110 115

gaa gag act ttt aag aaa tac aga gcg gag att tgagaattca tcgtgact 435
Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile
120 125 130

<210> 8

<211> 139

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: partial
sequence of pGEX2ThCD83ext

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Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Gly Thr Pro Glu
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Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro
10 15 20

Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu
25 30 35

Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
40 45 50 55

Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
60 65 70

Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
75 80 85

Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
90 95 100

Ser Gly Lys Val Ile Leu Arg Val Thr Gly Cys Pro Ala Gln Arg Lys
105 110 115

Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile
120 125 130

<210> 9

<211> 435

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: partial
sequence of pGEX2ThCD83ext_mut129_CtoS

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<221> CDS

<222> (1)..(417)
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 <222> (28)..(417)

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 Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro
 10 15 20
 tgg gat ccg cag gtt ccc tac acg gtc tcc tgg gtc aag tta ttg gag 144
 Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu
 25 30 35
 ggt ggt gaa gag agg atg gag aca ccc cag gaa gac cac ctc agg gga 192
 Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
 40 45 50 55
 cag cac tat cat cag aag ggg caa aat ggt tct ttc gac gcc ccc aat 240
 Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
 60 65 70
 gaa agg ccc tat tcc ctg aag atc cga aac act acc agc tgc aac tcg 288
 Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
 75 80 85
 ggg aca tac agg tgc act ctg cag gac ccg gat ggg cag aga aac cta 336
 Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
 90 95 100
 agt ggc aag gtg atc ttg aga gtg aca gga tcc cct gca cag cgt aaa 384
 Ser Gly Lys Val Ile Leu Arg Val Thr Gly Ser Pro Ala Gln Arg Lys
 105 110 115
 gaa gag act ttt aag aaa tac aga gcg gag att tgagaattca tcgtgact 435
 Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile
 120 125 130

<210> 10
 <211> 139
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: partial
 sequence of pGEX2ThCD83ext_mut129_CtoS

<400> 10
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 Val Lys Val Ala Cys Ser Glu Asp Val Asp Le